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                                                                 May 27, 2005, 08:27:23 ; Search time 161 Seconds (without alignments) 1054.583 Million cell updates/sec
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2325
1 MVSSAFAPSILLSLMSSLAL......TYARENGQGDFAKCGFVPSE 439
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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ALIGNMENTS

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6-Phytase; basidiomycetes; feed additive; feedstuff
                                                                                               1. .30
/label= Sig_peptide
31. .439
/label= Mat_protein
                                                                            Peniophora lycii, strain CBS 686.96
                                                                                         Location/Qualifiers
      AAW62858 standard; protein; 439 AA.
                                                                                                                                                                     96DK-0001481.
96DK-00001481.
97DK-0000301.
97DK-0000529.
97DK-00001388.
                                                                                                                                                        97WO-DK000568
                                                  Peniophora lycii 6-phytase
                                (revised)
(first entry)
                                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                     20-DEC-1996;
20-DEC-1996;
18-MAR-1997;
                                                                                                                                                         15-DEC-1997;
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01-DEC-1997;
                                                                                                                                WO9828409-A1
                               17-OCT-2003
09-NOV-1998
                                                                                                                                            02-JUL-1998
                   AAW62858;
                                                                                                            Protein
                                                                                               Peptide
AAW62858
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Phytase(s) from fungi of phylum Basidiomycota - useful as feed and food additives, e.g. to reduce phosphate content of manure and to improve digestibility.

Breinholt J, Fuglsang CC

Lassen SF, Bech L, Ohmann A,

WPI; 1998-377641/32. N-PSDB; AAV42331.

This polypeptide comprises a 6-phytase of the basidiomycete Peniophora lycii CBS 686.36. A cDNA clone (see AAV42331) encoding the enzyme was

Claim 25; Page 118-119; 197pp; English.

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in Aspergillus oryzae. The recombinant enzyme is very stable at 40 degc. In the pH range 3-9, and 50-60% of activity is retained after 1 hr at 60-60% degC; this may be due to the enzyme s ability to refold following thermal denaturation. The Peniophora phytase is more efficient than the known Aspergillus phytase in releasing inorganic phosphate from corn. It is essentially a 6-phytase. The invention provides basidiomycete phytases (see AAW62857-62), cloned DNA sequences (see AAV42330-35), processes for preparing the phytases, and their use especially as food or proparing the phytases, and their use especially as food or compared with known phytases, they show better heat stability or faster compared with known phytases, they show better heat stability or faster celease of phosphate from substrates, and may also show advantageous position specificaty and specific activity. They can be produced in commercially useful quantities. (Updated on 17-OCT-2003 to standardise OS
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   The 6-phytase has been expressed
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    MVSSAFAPSÍLLSLMSSLALSTOFSFVAAÖLPIPAONTSÍWGPYDPFFPVEPYAAPPEGC

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100.0%; Pred. No. 1.4e-224;
iive 0; Mismatches 0;
 obtained by expression cloning in yeast.
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Best Local Similarity
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The present sequence represents a polypeptide exhibiting phytase activity encoded by a cDNA derived from Peniophora lycil. This protein has been found to have superior properties to known phytases such as increased heat stability or faster release off phytate. The polypeptide produced can be used in e.g. liberating inorganic phosphate from phytate or phytic acid, in human food or animal feed preparations or in additives for such
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100.0%; Score 2325; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.4e-224;
Matches 439; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                              Claim 1; Page 54-57; 82pp; English.
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                           10-DEC-1997;
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us-10-734-510-7.rag

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The invention relates to novel active phytase variants (1) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manner, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents the phytase used in the invention.
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                       CPFDTLSSGNASPFCDLFTAEEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL
                                                                                       TGQAVRDETQTWRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE
                                                                                                                 TGQAVRDETQTINFTLDSDPATFPLINFFYADFSHDNTMVPIFAALGLFNATALDPLKPDE
                                                                                                                                                                                                  phytase; nutritional value; growth rate; weight gain; feed conversion.
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                                                                                                                                                                          NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT
CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL
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100.0%; Pred. No. 1.8e-217;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peniophora lycii phytase SEQ ID NO:2.
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                                                                                                                                                                                                                                                                  YARENGOGDFAKCGFVPSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the Peniphora lycii phytase sequence. The invention relates to variant phytase enzymes with specific amino acid substitutions for improved properties. The phytase variants can be used for inbrating phosphorus from a phytase substrate. They can be used for reducing phytate levels in animal manure. They can be used in feed or cod preparations. The phytase DNA can also be used in food or produce transgenic plants which can be used in feeds or foods. The phytase variants can also be used in soy processing and in the manufacture of inositol or derivatives. The phytase variants can have altered activities such as phystability, temperature stability, phy profile, temperature profile, specific activity (in particularly in relation to phy and temperature), substrate specificity, substrate cleavage pattern, substrate binding, sosition specificity, the velocity and level of release of phosphate from corn, reaction rate, phytase degradation rate and end level of released phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                       Phytase, variant, enzyme, phosphorus liberation; phytase substrate; phytate level reduction; animal manure; food preparation; soy processing; inositol manufacture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variant phytase enzymes, used for liberating phosphorus from a phytase substrate, for reducing phytate levels in animal manure and in feed and food preparations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC
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                                                              P. lycii phytase protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                               98DK-00000806.
98DK-00001176.
99DK-00000091.
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                       (first entry)
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(revised)
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18-SEP-1998;
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27-AUG-2003
                       07-DEC-1999
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Peniophora lycii phytase mutant (ii)
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                                                                                                  Best Local Similarity yy.o
Matches 422; Conservative
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Synthetic.
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                                                        Sequence 423 AA;
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                                                                                                                                     LFTAEEYVSYBYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The
                                          181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD
                                                                                                                                                       SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM
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                                                                               PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD
                                                                                                                                                                                                                                                                361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV
                            STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC
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30-SEP-2002; 2002DK-00001449
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Misc-difference 29
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| PSE 423
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present sequence represents a variant phytase of the invention. Note: ? present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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                                                                                                                                                                                                                                                                                                                              1 SLALSTQFSFVAAQLPIPAQNTSNWGPYSPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP
                                                                                                                                                                                                                                                                                                                                                                                                         77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ISGARSKQVAAVAKIQMARPPTDFKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY
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                                                                                                                                                                      96.7%; Score 2248; DB 7;
99.8%; Pred. No. 7.4e-217;
ive 0; Mismatches 1;
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Matches 421;
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                                                                                                                                            The invention relates to novel active phytase variants (I) with one or
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Pred. No. 9.3e-217;
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                                                                                                                   2; Page; 124pp; English.
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Best Local Similarity 99.5%;
Matches 421; Conservative
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                                   Matsui T, Fuglsang CC,
           (NOVO ) NOVOZYMES AS
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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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Pred. No. 1.2e-216;
0; Mismatches 2;
                                                                                                                                               /label= Wild-type A substituted
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                                                                                         Location/Qualifiers
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                                                                                                                                                                               Misc-difference 334
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Peniophora lycii
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Claim 2; Page; 124pp; English.
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30-SEP-2002; 2002DK-00001449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
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Pred. No. 1.2e-216;
0; Mismatches 1;
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                                                                                                                                                                                                                ..., Location/Qualifiers Misc-difference 330
                                                                       ADI66841 standard; protein; 423 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  plant material and manure.
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Best Local Similarity
Matches 422; Conserv
 439
                                                                                                                                                                                    Peniophora lycii.
Synthetic.
                   421 PSE 423
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                                                                                                                                                                    mutant; mutein.
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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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                                                                                                                                                                                         SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM
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PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD
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                                                                                                                                                                   TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY
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                                                                                         SLALSTQFSFVAAQLP1PAQNTSNWGPYDPFPPVEPYAAPPEGCTVTQVNL1QRHGARWP
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               Length 423;
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             Score 2246; DB 7;
Pred. No. 1.2e-216;
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               96.6%;
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                               Local Similarity 99.8
1e8 422; Conservative
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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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New phytase variants useful as animal feed additives and for treating plant material and manure.
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99.5%; Pred. No. 1.5e-216;
iive 0; Mismatches 2;
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                                                                                            Claim 2; Page; 124pp; English.
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Synthetic.
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ADI66781 standard; protein; 423 AA.
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          /label= Wild-type D substituted by
                                                                                                                                               Fukuyama S;
                                                                                                                                                Svendsen A,
                                                                                                                                                                                                                      Claim 2; Page; 124pp; English
                                                                       04-FEB-2003; 2003WO-DK000067.
                                                                                          08-FEB-2002; 2002DK-0000193
30-SEP-2002; 2002DK-00001449
                                                                                                                                               Matsui T, Fuglsang CC,
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Misc-difference 350
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12 RESULT

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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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                                                                                                     phytase; nutritional value; growth rate; weight gain; feed conversion;
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                                                                                                                                                                                                                                                                                                                 /label= Wild-type D substituted
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                                                 Peniophora lycii phytase mutant (vi)
                                                                                                                                                                                                                                                                Location/Qualifiers
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30-SEP-2002; 2002DK-00001449
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22-APR-2004 (first entry)
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                                                                                                                                 mutant; mutein
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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
                                                                  301 SDPATFPLARTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWYDSKLVPFSGHM 360
                                                    SDPATFPINRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
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                                                                                                      377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV
                                                                                                                     New phytase variants useful as animal feed additives and for treating plant material and manure.
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Length 423;

Score 2244; DB 7; Pred. No. 1.9e-216;

96.5%;

Query Match Best Local Similarity

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 Mismatches
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|PSE 423
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                                         The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in ADI66763.
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Pred. No. 1.9e-216;
0; Mismatches 2;
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                      Claim 2; Page; 124pp; English
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 plant material and manure.
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Best Local Similarity 99.5
Matches 421; Conservative
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The invention relates to novel active phytase variants (I) with one or more specific substitutions. The phytase variants of the invention are useful for improving the nutritional value of animal feed compositions (e.g. to increase growth rate, weight gain and/or feed conversion), reducing phytate levels in animal manure, treating vegetables or proteins, and liberating phosphorous from a phytase substrate. The present sequence represents a variant phytase of the invention. Note: The present sequence is not shown in the specification but is derived from the Peniophora lycii phytase sequence shown in AD166763.
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Best Local Similarity 99.5%; Pred. No. 2.3e-216;
Matches 421; Conservative 0; Mismatches 2;
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Wass M., Fuglsang C.C.;
Term four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a Ceriporia sp., and Trametes pubescens.";
Appl. Bruton. Microbiol. 67:4701-4707(2001).
REMBL, AJ310699; CAC48164.1; -.
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GO, GO:0008707; Ft-bytrase activity; IEA.
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                                                      360 VPNPWRTWRTSSLVPFSGRMVVBRLSCFGTTKVRVLVQDQVQPLEFCGGDRNGLCTLAKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG
                                                                                                                                                                                                                                                            KPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=phyA2;
cf. Ceriporia sp. CBS 100231.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Ceriporia.
NCBI_TaxID=154783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 1202; DB 2; Length 442; 52.6%; Pred. No. 2.4e-89; tive 61; Mismatches 128; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 442 Phytase.
442 AA; 47552 MW; 483FAB442DB001EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phytase precursor (EC 3.1.3.26).
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                                                                                                                                                                                                                                                                                                                                                                                                                   420 VESQTFARSDGAGDFEKC 437
                                                                                                                                                                                                                                                                                                                                                                                   416 VESQTYARENGQGDFAKC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 52.68
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                            357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96VK8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL
                                                                                                                                                                                                                                                                                                                                                                                   361 NRLWYDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESOT
                                                                                                241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL
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                                                                                                                                                                                                                                                                                                                                                361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cf. Ceriporia sp. CBS 100231.
Bukaryota, Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Ceriporia.
NCBI_TaxID=154783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bischoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CBS 100231;
Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R.,
Wyss M., Fuglsang C.C.;
Submitriced (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ310698; CAC48163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 442
442 AA; 47915 MW; 0464C1C691D86702 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phytase precursor (EC 3.1.3.26).
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GO; GO:0003933; F:acid phosphatase activity; IEA.
GO; GO:016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfan; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 YARENGOGDFAKCGFVPSE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 YARENGOGDFAKCGFVPSE 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=phyA1;
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Q96VK9
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122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VIQVNLIQRHGARWPISGARSRQVAAVAKIQMARPFIDPKYEFLNDFVYKFGVADLLPFG 121
                                                    NELLARLIGGAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA- 352
                                                                                                                                                                  LDPLKPDENRLMVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCE 411
181 VLSVIISEAGNDTLDDNMCPAAGDSDPQVNQWLAQFAPPMTARLNAGAPGANLTDTDTYN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SLFIGGCLLVFLQASAYGGVVQATFV--QPFFPPQIQDSWAAYTPYXPVQAYTPPPKDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ALGSSOAGEETFORYSFLVSKENLPFVRASSSNRVVDSATNWTEGFSAASHHVLNPILFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SAFAPSILLSLMSSLALS--TQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT
                             LMDMCPFDTLSSGNASPFCDLF---TAREYVSYEYYYDLDKYYGTGPGNALGPVQGVGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Agaricales; Bolbitiaceae; Agrocybe.
NCBI_TaxID=84607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 453 Phytase.
453 AA, 49931 MW; D62FIAEFA1091E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Q96VTO;
01-DEC-2001 (T-EMBLrel. 19, Created)
01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
101-DEC-2004 (T-EMBLrel. 26, Last annotation update)
Phytase precursor (EC 3.1.3.26).
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LDAFVESQAYARNDGEGDFEKC 440
                                                                                                                                                                                                                                     LSAFVESQTYARENGQGDFAKC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232; Conservative
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SEQUENCE FROM N.A.
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                                                                                                   294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 LPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 TLQVVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLMAAAPSANLSDSDALT 236
                                    241 CPFWTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTGYGQALGPVQGVGYINELLA 300
                                                                                                                                                    416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 EGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADL 117
                   CPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLA 298
                                                                                  299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21455028; PubMed=11571175;
DOI=10.1128/AEM.67.10.4701-4707.2001;
Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A., WASS M., Fuglsang C.C.

"Expression, gene cloning and characterization of five novel phytases from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a Ceriporia sp., and Trametes pubescens.";
Appl. Environ. Microbiol. 67:4701-4707(2001).

EMBL; AJ310700; CA448234.1; --
HSSP; P34752; IIHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 SILLSLMSSLALSTQFSFVAAQLPIPAQNTS-----NWGPYDPFFPVEPYAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Trametes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.9%; Score 1160; DB 2; Length 443; 52.0%; Pred. No. 6.3e-86; tive 63; Mismatches 127; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 443 Phytase.
443 AA; 47773 MW; 13D4BEBCE0B049D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phytase precursor (EC 3.1.3.26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P34722; IHP.

GO; GO:0008707; F:4-phytage activity; IEA.

GO; GO:000393; F:acid phosphatase activity; IEA.

GO:000.001697; F:hydrolase activity; IEA.

InterPro; IPR00560; HisAc_phsphtse.

Pfam; PF00328; Acid_phosphat_A. 1.

PROSITE; PS00516; HIS_ACID_PHOSPHAT_1; 1.
                                                                                                                                                                                                                                                                                                                                           443 AA.
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                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                       433
                                                                                                                                                                                                                                                     421 ESOAYARSGGAGDPEKC 437
                                                                                                                                                                                                                       417 ESOTYARENGOGDFAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.0%
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trametes pubescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=154538;
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                                                                                                                         419
                                                      CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
                                                                          360 ENRLWUDSKLVPFSGHMTVEKLAC----SG-----KEAVRVLVNDAVQPLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from phytate.
-[-CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)0 = 1D-myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
-[-SUBCELLULAR LOCATION: Secreted.
-[-MISCELLANBOUS: Shows activity with phytic acid at a pH range of 3.5 to 8.5, with maximal activity between pH 5.5 and 6.0. Also accept 4-nitrophenyl phosphate as substrate with a pH optima shifted to more acidic pH values.
-[-SIMILARITY: Belongs to the histidine acid phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fundi Aspergillus terreus and Myceliophthora thermophila.", Microbiology 143:245-252 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate phosphohydrolase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thielavia heterothallica (Myceliophthora thermophila).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Corynascus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=97177792; PubMed=9025298;
Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
van Loon A.P.G.M.;
                                                                                                                                                                                                                                                                        433
                                                                                                                                                                                                                                                                                       420 CGGDMDSLCTLEAFVESQKYAREDGGGDFEKC 451
                                                                                                                                                                                                                                                                     CGG-VDGVCELSAFVESQTYARENGOGDFAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U59806; AAB52508.1;
HSSP; P34752; IIHP.
InterPro, PR000560; HisAc_phsphtse.
Pfam. PF0028; Acid_phosphat A; 1.
PROSITE; PS00616; HIS ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              487
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Poly-Gly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 GTSTNRTLDGDPRTFPLGRPLYADFSHDNDMMGVLGALGAND--GVPPLDKTARRDFEEL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 GRPLSPFCRLFSESSEWRAYDYLQSVGKWYGYGPGNPLGPTQGVGFVNELLARLAGVPVRD
                                                                                                                                                                                                                                       WGPYDPFF -- PVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFT
                                                                                                                                                                                                                                                                                                                                                   SSTINMTAGEGDA----SGETVLPTL---QVVLQEE--GNCTLCNNMC-----PNEVDGD
                                                                                                                                                                                                                                                                                                                                                                   251 A---SPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 RLWVDSKLVPFSGHMTVEKLACSG------KEAVRVLVNDAVQPLEFCGGV
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus ficuum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
              Proton donor (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                               58;
                                                                                                                                                                                   Length 487;
                                                                                                                                                                                35.4%; Score 823; DB 1; Length 487, 43.2%; Pred. No. 2.1e-58; ive 52; Mismatches 142; Indels
    Nucleophile (By similarity). Proton donor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                        ES-TIWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang L., An L., Wang Y., Yuan X.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY01315, AG40895.1; -.
HSSP; P34752, 11HP.
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR00560; HisAc phsphtse.
Pfam; PF00328; Acid phosphat 1; 1.
PROSITE; PS00616; HIS ACID PHOSPHAT_2; 1.
                                                                                                                                                         97D10EDC83D051DB CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                            Matches 192; Conservative
369
369
26
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ACT_SITE
ACT_SITE
DISULFID
                                                       DISULFID
                                                                                                            CARBOHYD
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                                                                                 DISULFID
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"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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                                                            preliminary data.
             Nature 0:0-0(2003).
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                                                                                                                                                                              Hypothetical
SEQUENCE 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Jaffe D., FitzHugh W., Ma L.J., Smirnov S., Purcell S., Rehman B.,
BIKins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Pedersen D., Nelsen C.B., Butler J., Endrizzi M.,
A Selitrennikoff C.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
A Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A raden O., Plaamn M., Seller S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
A Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
                                                                                                                                                                                                                          EVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----SPF 254
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                                                                                                                                                                                                                                                                   160 STNWTAGF------GDASGETVLPTLQVVLQE------EGNCTLCNNMCPN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 TVPPASRMYVEMMQCQSEQEPLVRVLVNDRVVPLHCC-PVDALGRCTRDSFVRGLSPARS 458
                                                                                                                                                                                                                                                                                               170 GNKFIEGFØSTKLKDPRAQPGQSS----PKIDVVISBASTSNNTLDPGTCTVFED---S 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE 424
                                                                                         43
                                                                                                         44 YDPFFPVEPYAA----PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 LDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFSSAR
                                                                                        2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA---QNTSN-------WGP
                                                            Gaps
                                                          83;
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                             Length 467;
                           Query Match 33.4%; Score 776.5; DB 2; Length Best Local Similarity 38.4%; Pred. No. 1.2e-54; Matches 188; Conservative 62; Mismatches 156; Indels
51012 MW; 3F69AD543C0B565B CRC64;
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459 G--GDWAEC 465
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 467 AA;
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MEDLINE=98007872; PubMed=9349716; DOI=10.1016/S0167-4781(97)00107-3;
Passamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
Van Loon A.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.3%; Score 773.5; DB 2; Length 596; Best Local Similarity 37.6%; Pred. No. 2.9e-54; Matches 195; Conservative 65; Mismatches 158; Indels 101
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Eurotiales, Trichocomaceae, Talaromyces.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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596 AA; 65281 MW; 7085B991224AE410 CRC64;
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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HSSP, P34752; 11HP.
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc_phopptse.
Pfam, P00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR.2004 (TrEMBLrel. 26, Phytase (EC 3.1.3.8).
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                                                                                                                                                                                            96 PFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQR
                                                                                                                                                                                                                             156 VVDSSTNWTAGFGDASGETVL-----PTLQVVLQEEG---NCTLCNNMCPNEVDG
                                                                                                                                                                                                                                                             203 ----DESTIWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---SPFC
                                                                                                                                                                                                                                                                                                                                                              368 KLVPFSGHMTVEKLAC--SGKEAVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYAR
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                              48;
                                                                                                                              Length 466;
                                                                                                                                             49; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SK-57;
Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB022700; BAA74433.1; -.
HSSP; P34752; IIHP.
GO; GO:0003993; F:acid phosphatase activity; IEA.
                                                                                                             466 AA; 51450 MW; FC4575B521A5C929 CRC64;
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Last annotation update)
                                                                                                                           33.1%; Score 769; DB 2; 42.8%; Pred. No. 4.9e-54;
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                                                                                                                                    Best Local Similarity 42.0%;
Matches 184; Conservative
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01-MAY-1999 (TrEMBLrel. 10
01-MAX-2004 (TrEMBLrel. 20
Phytase.
Name=phyA;
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454 QGGNWEGCYA 463
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                                                                                                    Hydrolase.
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                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                               160 STINWIAGF------EGNCTLCNNMCPN
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                                                                                                                                                                                                                                                                                                                     44 YDPFFPVEPYAA----PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5058;
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                                                                                                                                         Length 467;
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EMBL; AFS37344; AAN10115.1; -.
HSSP, PAT52; ILTHP
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR00556; HisAc_Dapphtse.
Pfam; PF00228; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
NON TER
SEQÜENCE 448 AA, 49260 MW; 0554FF9712FF7BAA CRC64;
                                                                                                                                                                                 Indels
                     Pfam; PF00328; Acid_phosphat_A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SROUENCE 467 AA; 51028 WW; 7A38AD543EDC265C CRC64;
                                                                                                                                                                                                                              2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA---QNTSN-
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Last sequence update)
Last annotation update)
                                                                                                                                    33.0%; Score 767.5; DB 2;
38.2%; Pred. No. 6.5e-54;
cive 61; Mismatches 158;
InterPro; IPR000560; HisAc phsphtse.
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01-WAR-2003 (TEMBLE1. 23,
                                                                                                                                                                              Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phytase (Fragment).
                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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167

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SHDNIMISVFFALGLYNIT--EPLSOISVOSIEEINGYSSARIVPFGARAYVEMMOCIDE 416
SSLSEDVPDHCQVTPAQVLSRHGARYPTKSKSEKYAKLIKAVQHNATSFSGKYAFLKSYN 119
                                                                   SHDNTMVPIFAALGLFNATALDPL-----KPDENRLWVDSKLVPFSGHMTVEKLACSGK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 VDSSTNWTAGF------GDASGETVLPTLQVVLQE------EGNCTLCNNM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGF--
                                                                                                                             217 TARLNAAAPSANLSDSDALTLMDMCPFDTLS----SGNASPFCDLFTAEEYVSYEYYYDL
                                                                                                                                                                                                 DKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADF
                                                                                                                                                                                                                                                           299 SKYYGYGGGNPLGPAQGIGFANELIARLIKSPVKDHTTINTTLDSNPATFPLNATLYADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 WGPYDPFFPVEPYAA----PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 WGQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 FIDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 TPEGKYAFLKTYDYSLGADDLTPFGEGELVNSGVKFYQRYESLTR-NIVPFIRSSGSSRV
                                                                                                              ---GDASGE--TVLPTLQVVLQE-EG-NCTLCNNMC---PNEVDGDES-TTWLGVFAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                            KEPLVRVLVNDRVIPLQGCDADEYGRCKRDDFVEGLSFVTSG--GNWGEC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                          E--AVRVLVNDAVQPLEFCGGVD-GVCELSAFVESQTYARENGQGDFAKC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.7%; Score 760.5; DB 2; Length 448; 40.5%; Pred. No. 2.3e-53; ative 56; Migmatches 148; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu J., Yan C.Y., Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL; ARGISTIZ, AATS1735.1; -
GO, GO:016158; F:3-phytase activity; IEA.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:001677; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 AA; 49170 MW; C319E1FECEB4EF18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last 05-JUL-2004 (TrEMBLrel. 27, Last Phytase (EC 3.1.3.8) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 175; Conservative
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Q6GYA8
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                                                                                                                                                                                                              .-----GDASGETVLPTLQVVLQE------EGNCTLCNNM 195
                                                                                                                                                                                                                                            201
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                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AA----PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
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                                                                              41 WGPYDPFFPVEPYAA----PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP 96
                                                                                                             88
                                                                                                   29 WGQYAPPFSLANKSAISPDVPAGCQVTFAQVLSRHGARYPTDSKGKKYSALIEEIQONAT
                                                                                                                                                               378 SAWIVPFASRMYVEWMQCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCIRDSFVKGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 FTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV
                                                                                                                                                                                                                                          148 IASGNKFIEGPQSTKLKDPRAQPGQSS----PKIDVVISEASTSNNTLDPGTCTVFED-
                                                                                                                                                                                                                                                                            CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----
                                                                                                                                                                                                                                                                                                                                          SPFCDLFTAEEYVSYBYYYDLDKYYGTGPGNALGPVQGVGYVNBLLARLTGQAVRDETQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 -SKLVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SILLSLMSSLALSTQFSFVAAQLPIPAQNTSN--------WGPYDPFFPVEPY
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                53;
                  DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 466;
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32.9%; Score 765.5; DB 2; Length 'Best Local Similarity 38.1%; Pred. No. 9.4e-54;
Matches 179; Conservative 65; Mismatches 171; Indels
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gomi K.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, BA0420805; BAB40715.1; -.
HSSP; P34752; 11HP.
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Ffam; PF00328; Acid phosphat A; 1.
PROSITE; PS00016; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SEQUENCE 466 AA; 51257 WW; 8033BED57FBA279I CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
               32.9%; Score 765.5; DB 2;
40.7%; Pred. No. 8.9e-54;
live 55; Mismatches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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01-JUN-2001 (TrEMBLrel: 17,
01-JUN-2001 (TrEMBLrel: 17,
01-MAR-2004 (TrEMBLrel: 26,
             Query Match 32.9
Best Local Similarity 40.7
Matches 176; Conservative
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ARSG--GDWAEC 446
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Name=phyA;
Aspergillus oryzae.
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Q9C1T1
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Aspergillus ficuum phytase.";
Biochem. Biophys. Res. Commun. 178:45-53(1991)
                                                                                                                                                                                                                                                                                                                       467 AA
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STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
MEDLINE=89160685; PubMed=2852807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene (phyA) of Aspergillus niger.";
Gene 127:87-94(1993).
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                       422 ARENGOGDFAKC 433
                                                                                                                                                                                     ARSG--GDWGEC 446
                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5061;
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P34752;
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PHYA ASPNG
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          251
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                                                                                                                                                                                                                                            421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 TPEGKYAFLKTYNYSLGADDLTPFGEQELVNSGVKFYQRYESLTR-NIVPFIRSSGSSRV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 VDSSTNWTAGF-----GDASGETVLPTLQVVLQE------EGNCTLCNNM 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
196 CPNEVDGDESTTWLGVFAPNITARLINAAAPSANLSDSDALTLMDMCPFDTLSSGNA----
                                                                                                       SPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQT
                                                                                                                                  378 SAWTVPFASRMYVEMMQCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVKGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 WGQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Nong Y., He Y., Rachid L., Wu Z., Qing Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY603416, AAT12504.1;
GO; GO:0003993; F:acid phosphatase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA; 49169 MW; FBABFCDE20140514 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 AA
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Pfam, PF00328; Acid_phosphat_A; 1.
PROSITE; PS00616; HIS ACID_PHOSPHAT_1; 1.
NON TER.
SEQÜENCE 448 AA; 49169 MW; FBABFCDE201
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Aspergillus oryzae.
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Matches 175; Conserv
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05-JUL-2004
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320 NHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFS 377
                                                                                     367 -SKLVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY 421
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STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
MEDLINE=92249451; PubMed=8387289;
Ullah A.H.J., Dischinger H.C. Jr.;
"Appergillus ficuum phytase: complete primary structure elucidation by chemical sequencing.";
                                                                                                                                           378 SAWITVPPASRMYVEMMQCQSEQEPLVRVLVNDRVVVPLHGC-PVDALGRCTRDSFVKGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
MEDLINE=92352284; PubMed=8387447; DOI=10.1016/0378-1119(93)90620-I;
Wan Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M., Gouka R.J.,
Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A., Selten G.C.M.,
Veenstra A.E., van Gorcom R.F.M., van den Hondel C.A.M.J.J.;
"Cloning, characterization and overexpression of the phytase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
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"Aspergillus ficuum phytase: partial primary structure, substrate
selectivity, and kinetic characterization.";
Prep. Biochem. 18:459-471(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FCB-1994 (Rel. 45, Last amoutation update)
3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate phosphohydrolase A).
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STALAIN-RREL 3135 / Van Tieghem / Ficuum;

MEDLINE=97307250; PubMed=9164457;

Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell

Wan Loon A.P.G.M.;

"Crystal structure of phytase from Aspergillus ficuum at 2.5-A
resolution.";
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MEDLINE=91298982; PubMed=1648914;
Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;
"Cyclohexanedione modification of arginine at the active site
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"Sequence of the Aspergillus niger (ficuum) phytase gene
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
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160 STNWTAGF------EGDASGETVLPTLOVVLOE------EGNCTLCNNMCPN 198
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38.2%; Pred. No. 2.9e-53;
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                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               from phytate.

CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)0 = 1D-CATALYTIC ACTIVITY: Myo-inositol 1.2,4.5,6-pentakisphosphate + phosphate.

SUBCELLUTAR LOCATION: Secreted.

BIOTECHNOLOGY: Is used as a food and feed additive. It can facilitate the degradation of phytin in soybean and other seeds used as food for monogastric animals. Sold by Novo Nordisk under the name Phytase Novo.

SIMILARITY: Belongs to the histidine acid phosphatase family.
Struct. Biol. 4:185-190(1997). FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
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PIR; JN0656; JN0656.
PDB; IHP; X-ray; G. 30-467.
InterPro; IPR000560; HisAc_phsphtse.
PRO3128; Acid_phosphat_A; I.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_2; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
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Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	(EC 3		3-phytase (EC 3.1.	phata	thiamin-repressibl	acid phosphatase (acid phosphatase (acid phosphatase (acid phosphatase (hypothetical prote	histidine acid pho	hypothetical prote				_	yfaL protein - Esc	acid phosphatase (hypothetical prote	aspartic proteinas	probable arginine-	intrinsic factor-B	sulfite reductase	cellobiose oxidase
SUMMARIES	ΙD	N065	JN0889	JN0482	S14119	T39929	A25326	JC4285	JN0715	00890	PABYC	PABYCC	S52495	S53476	848996	A86233	JE0369	S75251	A83412	D91018	F85862	D88504	G64993	S64682	T16883	S52783	T40535	T08618	H81110	860676
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	Query Match Length	467	467	441	463	463	453	468	479	479	467	467	468	467	467	468	465	3972	2468	1250	1250	411	1250	438	380	397	415	3623	604	770
de	Query Match		32.5	32.0	17.7	16.8	16.8	16.6	15.1	15.0	14.9	14.4	14.3	13.6	13.4	7.0	6.8	4.6	4.5	4.5	4.5	4.4	4.4	4.3	4.3	4.3	4.3	4.2	4.1	4.1
	Score	59	754.5	743.5	412	390.5	390	385	351	348	345.5	335.5	331.5	315.5	312.5	162.5	159	107.5	104	103.5	103.5	101.5	101.5	101	100	66	66	ů.	95.5	95.5
	Result No.		7	m	4	2	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

199 EVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----SPF 254

: || | | | : | | 1.0 GKKFIEGFQSTKLXDPRAQPGQSS-----PKIDVVISEASSSNNTLDPGTCTVFED---S 221

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hypothetical prote	hypothetical prote	hypothetical Ber-r	DNA polymerase III	probable fibrillin	hypothetical prote	fhuD protein (AJ00	probable hydrolase	hypothetical prote	hypothetical prote	probable peptidogl	hypothetical prote	peroxidase (EC 1.1	aldehyde oxidase (aspartic proteinas	NADPH-cytochrome P	
D86897	B86748	T41060	H75511	C84769	AB3051	B98235	T37132	T20893	AG2293	AE1525	T23024	T09565	T51623	S64958	JE0230	
~	~	~	N	~	~	N	~	~	7	~	N	~	7	~	7	
926	1093	626	1335	376	293	300	401	408	533	629	1332	343	1321	508	713	
4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	
95.5	95.5	95	94.5	93.5	93	93	93	93	93	93	93	92.5	92.5	92	92	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT	LT 1
JN0656 3-phyte	JN0656 3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger N.31ternamen mwo-inosirol hexakisnhosnhate nhosnhohvdrolase: phvA protein
is to	C.; Species: Aspergillus niger C.; Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C; Ac R; V6	C;Accession: JN0656; S28456 R;van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.F
A.M.	A.M.J.J.
A;Tj	At Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)
A;R¢	A;Reference number: JN0656; MUID:93252284; PMID:838/44/ A;Accession: JN0656
A;MC	A:Molecule type: DNA A:Regidings: 1-467 <van></van>
A,C	A; Cross-references: UNIPROT: P34752; GB: Z16414; NID: 92392; PIDN: CAA78904.1; PID: 92393
A,E	A, Experimental gource: strain NRRL3135
A;N	A;Note: parts of the sequence, including the amino end of the mature protein, were confil C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and ino
300	C;Genetics:
A; Ge	A,Gene: phyA
H.C.	Aşintrons: 157. C.Sminorfamily. Voset arid nhoenharase
20,0	o, servards: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosphore
F;1-	23/Domain: signal sequence #status predicted <sig></sig>
F;24	F:24-467/Product: 3-phytase A #status experimental <mat></mat>
F 81	1361/Active site: Arq, His #status predicted
F; 8;	F;82/Active site: His (phosphohistidine intermediate) #status predicted
б і	
M B	Best Local Similarity 38.2%; Pred. No. 9.5e-54; Matches 187; Conservative 58; Mismatches 161; Indels 83; Gaps 18;
ò	2 VSSAPAPSILLSLMSSLALSTQFSPVAAQLPIPA-QNTSNWGP 43
q	:
à	44 YDPFPPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD 99
ą	

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A;Molecule type: protein
A;Residues: 1-441 <ULL>
A;Cross-references: UNIPROT:P34752
A;Cross-references: UNIPROT:P34752
A;Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
B;Ochem. Biophys. Res. Commun. 178, 45-53, 1991
A;Title: Cyclohexanedione modification of arginine at the active site of Aspergillus ficu
A;Reference number: PN0023; MUID:91298982; PMID:1648914
A;Accession: PN0023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 48-70 cUL2.
C;Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate.
C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;58,338/Active site: Arg, His #status predicted
F;58,338/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NiAlternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein CiSpecies Aspergilus ficuum CjSpecies: Aspergilus ficuum CjDate: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 CjAccession: JN0482; PN0023 R;Ullah, A.H.J.; Dischinger Jr., H.C. R;Ullah, A.H.J.; Dischinger Jr., H.C. A;Tille: Aspergilus ficuum phytase: Commun. 192, 747-753, 1993 A;Tille: Aspergilus ficuum phytase: Complete primary structure elucidation by chemical A;Reference number: JN0482; MUID:93249451; PMID:8387289
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                                                                                        368
CDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHT 341
                                                                                                                                                                                                         424
                                                                                                                                                                                                                                      400 TVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PIDALGRCTRDSFVRGLSFARS 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 NHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTTVENITQTDGFS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                      342 LDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTTVENITOTDGFSSAW
                                                                                                                                                                                                      LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 WGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 SPFCDLFTHDEWINYDYLOSIKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 WGPYDPFFPV--EPYAAP--PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 FTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 VDSSTNWTAGF------EGNCTLCUNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 IASGKKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASSSNNTLDPGTCTVFED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPFCDLFTAEEYVSYRYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.0%; Score 743.5; DB 1;
40.4%; Pred. No. 1.8e-52;
ative 53; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-phytase (EC 3.1.3.8) A - Aspergillus ficuum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.4 Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                   425 NGQGDFAKC 433
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459 G--GDWAEC 465
                                                                                                                                                                                                      369
                                282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
Nalternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: Jubess
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A;Fitle: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A;Accession: JN0889; MUID:94040796; PMID:8224894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-467 < PID>
A; Cross=references: Untra01: 134753; GB:L02421; NID:g166518; PIDN:AAA16898.1; PID:g166519
A; Experimental source: strain ALK0243
A; Note: part of the sequence, including the amino end of the mature protein, was confirm C; Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic pho C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphatase
C; Reywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp F; 1-19/Domain: signal sequence #status experimental < VAT>
F; 20-467/Product: 3-phytase A #status experimental < VAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-46/Product: 3-phytase A #status experimental <MAT>
F;27,59,105,120,207,230,335,352,376,388/Binding site: carbohydrate (Asn) (covalent) #sta
F;81,361/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                     282 CDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANBLIARLTHSPVHDDTSSNHT 341
                                                                                                                                                                     LDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD----SK 368
                                                                                                                                                                                                         110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
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ELADIVEANFIATFVPSIRQRLENDLSGVTLIDTEVTYLMDMCSFDTISTSTVDTKLSPF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
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                                                                                                                                                                                                                                                                                                                   400 TVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVRGLSFARS
                                                        CDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRT
                                                                                                                                                                                                                                                                                   369 LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VSAVLLPLYLL------AGVTSGLAVPASRNOSTCDTVDQGYQCFSETSHLWGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---SPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA---QNTSN----
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G--GDWAEC 465
                                                                                                                                                                                                                                                                                                                                                                                                   425 NGQGDFAKC 433
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В ઠે 셤

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acid_phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25345, TSGA65
C;Accession: A25345, TSGA65
J. Biol. Chem. 261, 2936-2941, 1986
A;Title: Isolation and characterization of the structural gene for secreted acid phosphat A;Reference number: A25326
A;Reference number: A25326
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-463 <LYN>
A;Cross-references: UNIPROT:060172; EMBL:AL023286; PIDN:CAA18863.1; GSPDB:GN00067; SPDB::
A;Experimental source: strain 972h-; cosmid c21H7
                                                                                                                                                                 (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNCTLCN-----NMCP------NEVDGDESTTWLGVFAPNITARLNAAAPSA-NLSD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDALTIMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 TPQNPLPTDKNIYTYSQKTSSFVPFAGNLITELFFCSDSKYYVRHLVNQQVYPLIDCGYG 417
                                                                                                                                                                 thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pc
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 LGRQLYQRYYKLFD-SYVYDINTAEQERVVESAKWFTYGLFGDKMYEKT----NFILISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ----SQYLNNFQEKLLNGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSRGRLELFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 TGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAG-FGDASGETVLPTLQVVLQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPYDPFFPVEPY-----AAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 GTLSPYH--EPYFDGLDSAFPETCEIQQVHLLQRHGSRNPTGDVTATDVYS-----
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                                                                                                                                                                                                                                             C;Accession: T39929
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, submitted to the EMBL Data Library, May 1998
A;Reference number: Z21857
A;Accession: T39920
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 16.8%; Score 390.5; DB 2; Best Local Similarity 28.4%; Pred. No. 8.4e-24; Matches 127; Conservative 60; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 FTDPKYEFLNDFVYKF------
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C,Superfamily: yeast acid phosphatase
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440 STSNGIANFNSQC 452
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                                                                                                                                                                                                                                                                                                                  acid phosphatase (BC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S14119; T40455
R;Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A;Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosa A;Reference number: S14119; MUID:91064763; PMID:2249257
A;Scatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-463 <YAN>
A;Cross-references: UNIPROT:Q01682; GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
A;Cross-references: UNIPROT:Q01682; GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
aubmitted to the EMBL Data Library, November 1998
A;Reference number: Z21931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN: CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 PUNFSYPENPLY-FVKHWTPVIKAENADQLSSSGRIELFDLGRQVFERYYELFD-TDVYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 NIDENTTEAAHTSWRNVFLKPIANRLNKYFDSGYNLTVSDVRSLYYICVYEIALRDN-SD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 ASD------RKVFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDKNIFTYSLKTSSF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 PFT-----DPKYEFLNDF--VYKFGVAD-LLPFGANQSHQTGTDMYTRYSTLFEGGDVPF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 VRAAGDQRVVDSSTNWTAG-FGDASGETVLPTLQVVLQEE----GNCTLCNNMCPNEVDG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 -- DESTI-----WLGVFAPNITARLINAAAPSA-NLSDSDALTLMDMCPFDTLSSGNASP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNR 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                            374 SAWIVPFASKLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PVDALGRCIRDSFVRGLSF
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17.7%; Score 412; DB 2;
Best Local Similarity 32.6%; Pred. No. 1.5e-25;
Matches 141; Conservative 58; Mismatches 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T40455
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-463 <LYN>;
fCross-references: EMED:AL034382; PIDN:CAA22278.
Experimental source: strain 972h-; cosmid C428
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                                                                                                                                       422 ARENGOGDFAK 432
                                                                                                                                                                                           433 ARSG--GDWAE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
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C; Superfamily: yeast acid phosphatase
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             A;Cross-references: UNIPROT:P08091; GB:M11857; NID:9173422; PIDN:AAA35321.1; PID:9173423
R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
                                                                                                                                                    GSPDB:GN00067; SPDB:SPBP4G3.02
                                                                                                                                                                                                                                                                                                                                                                               22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AAN-----ADALSSSGRVELFDMGRQFYERYHELFNASTYNIYTAA-QQRVVDSAL- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *-YGYG-MFGEDVHNFTNYILVSENATAGSNSLSSYNACPAS-DADDFTTPALEAWRNVY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272
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                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                     Map position: 2 scid phosphatase Superfamily: yeast acid phosphatase (Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase; 68/Active site: Arg #status predicted; 69/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FLONLFLGFLAVVCANAQPARFTAFDGKFDFKEHLTSRSPYHKPYF-YGPSIDFPTTCKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KQVHTLQRHGSRNPTGGNAAFDAVGIANFOORLLNGSVPIDYSVSGNPLSFVPTWTPVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 APNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 MPPIRQRLNPYFSNYNLTNDDILNLYGICSYE-IALQDYSEFCKLFNSVDFLNFEYEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| ::|: ||| |: | :|| | :| THDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMKASEFVPPAGNLITELFQCEDSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOVNLIORHGARWPTSGARSROVAAVAKIOMAR-----------PFTDPKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 FLNDFVYKRGVADLL-PFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTAGFGDASGETVLPTLQVVLQEE-----GNCTLCNNMCPNEVDGDESTT-----WLGVF
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                                                                                                                                                                                                                                                                                                                                                                                                                6 FAPSILLSLMSSLALSTOFS-FVA--AQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTV
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                             78;
                                                                                                                                                                                                                                                                                                                                          Length 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
16.8%; Score 390; DB 1; Length 45
Best Local Similarity 29.7%; Pred. No. 8.9e-24;
Matches 138; Conservative 58; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 AVRVLVNDAVQPLEFCG----GVDGVCELSAFVESQTYARENG 426
                                                                A.Reference number: 225068
A.Accession: T50405
A.Molecule type: DMA
Fresidues: 1-453 <RIE>
A.Cross-references: EMBL:AL137099; PIDN:CAB68657.1; CA.Experimental source: strain 972h(-); clone pl p4G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 SFSYGMGNSVKWGSIFGGAYANSLANSL--RSVENNTQ-
                                                                                                                                                                                 Genetics:
Gene: phol; SPDB:SPBP4G3.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho C;Species: Pichia pastoris
C;Date: 14-Nov_1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
RESULT 7
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hydrolae
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrole F;1-15/Domain: signal sequence #status predicted <SIG>F;1-15/Domain: acid phosphatase #status predicted <MAT>F;84/Active site: His (phosphohistidine intermediate) #status predicted F;165,136,1360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted F;345/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 PQD--YDYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRERYDHLINTSEEGKKLSVWAG 176
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                                                                                                                                                                                                                                                                                                                                                                     60 NGWGIAAESEIESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGP-LSF
                                                                                                                                                                                                                                                                                 LNDFVYKFGVADLLPF-----GANQSHQTGTDMYTRYSTLF---EGGDVPFVRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESTIWLGVPAPNITA-----RINAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FPNDIAEREADRIATISPGFNITADDIPTIALYCGFELNVRGESS-FCDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 FTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 ISREALLYTAYLRDLGWYYNVGNGNPLGKTIGYVYAN------ATR---QLLENTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPATFPLINRTFYADFSHDNTMVPI FAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 DPRDYPL----YFSFSHDTDLLQVFTSLGLFNVTDLPLDQTGFQTSFKSTEIVFMGARLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 VEKLACS--GKEA--VRVLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQGDFAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAPSILLSIMSSLALSTQFSFVAAQL-----PIPAONTSNWGPYDPFFPVEPY---
                                                                                                                                                                                                                                                                                                                                           -----AAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMA--RPFTDPKYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 GDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEG----NCTLCNNMCPN----EVDG
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          90;
                                                                                                                                                              Length 468;
                                                                                                                                                                                                          Indels
                                                                                                                                                              ; Score 385; DB 2; L; Pred. No. 2.4e-23; 61; Mismatches 192;
                                                                                                                                                          16.6%;
                                                                                                                                                                                   Best Local Similarity 29.4 Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CGFVP 437
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                                                                                                                                                              Query Match
Best Local Similarity
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J-phytase (EC 3.1.3.8) B precursor - Aspergillus ficuum
N.Alternate names: pH 2.5-optimum acid phosphatase
C;Species: Aspergillus ficuum
C;Species: Aspergillus ficuum
C;Species: Anoli-1994 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0715; RN0594; PN0460
R;Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem: Biophys. Res. Commun. 195, 53-57, 1993
A;Tile: Identification and cloning of a second phytase gene (phyB) from Aspergillus nige
A;Reference number: JN0715; MuID:93371452; PMID:7916610

A;Molecule type: DNA A;Residues: 1-479 <EHR> A;Cross-references: UNIPROT:P81440; GB:L20567 A;Accession: PN0594 A;Molecule type: protein A;Residues: 20-101;133-146;376-399 <EH2>

Riullah, A.H.J.; Dischinger Jr., H.C. Blachem. Blopbyse. Res. Commun. 192, 754-759, 1993 A.Fille: Identification of active-site residues in Aspergillus ficuum extracellular pH A;Reference number: PN0460; MUID:93249452; PMID:8484781 A;Accession: PN0460 A;Molecule type: protein

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Query Match
Best Local Similarity 27.24
Matches 128; Conservative
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A; Residues: 65-66,68-93 
    Comment: This enzyme, previously characterized as an acid phosphatase (EC S.Comment: This enzyme, previously characterized as an acid phosphatase
    C; Genetics:
        A; Gene: phys
    A; Introns: 261/1; 300/2; 335/2
    C; Superfamily: yeast acid phosphatase
    C; Superfamily: yeast acid phosphatase
    C; Superfamily: yeast acid phosphatase
    C; Superfamily: phosphopistidine; phosphopistidine; phosphopistidine; phosphopistidine intermediate
    F; 1-19/Domain: signal sequence #status predicted <SIG>
    F; 1-19/Domain: signal sequence #status predicted <AIG, His #status predicted</li>
    F; 81,337/Active site: Arg, His #status predicted
    F; 81,337/Active site: His (phosphohistidine intermediate) #status predicted
    F; 106,191,227,250,315,340,425,442,458/Bsinding site: carbohydrate (Asn) (covalent) #status

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: yeast acid phosphatase
Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; I
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; I
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optine. A;Reference number: JN0889; MUID:94040796; PMID:8224894
                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 VDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN-EVDGDESTTWLGVFAPN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 IETARKFGEGF----FGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTT-----CDN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 IT-----ARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPF---CDLFTAEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 YVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 PLNRIFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD------SKLVPF 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 NL------AHDTNITPILALGV-----LIPNED-LPLDRVAFGNPYSIGNIVPM 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 --PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE--FLNDFVYK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLTLACALATGASAFSYGAA-IPQSTQEKQFSQEFRDGYSILKHYGGNGPYSERVSYGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ILSLMSSLAL-STQFSFVAAQLPIPAQN------TSNWGPYDPFFPVEPYAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 FGVADLLP-------FGANQSHQTGTDMYTRYSTLFEGGD-VPFVRAAGDQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%; Score 351; DB 1; Length 479; 27.9%; Pred. No. 1.4e-20; Live 68; Mismatches 157; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 SGHMITVEKLACSGKEA-----VRVLVNDAVQPLEFCGGVDGV-CELSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 261/1; 300/2; 335/2
                                                                                                                                                                                                                                                                                                                                   Query Match 15.19
Best Local Similarity 27.9
Matches 131; Conservative
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A;Residues: 1-479 <PID>
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acid phosphatase (BC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisiae)
NyAlternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 19-Feb-1884 #sequence revision 30-Sep-1891 #text change 09-Jul-2004
C;Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A277; R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast A; Reference number: S05794; MUID:85037940; PMID:6093051
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #status
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A;Molecule type: DNA
A;Residues: 1-467 < EBAJ:
A;Cross-references: UNIPROT:P00635; EMBL:X01079; NID:g4162; PIDN:CAA25555.1; PID:g758282
A;Note: the authors translated the codon TAC for residue 272 as Thr
A;Accession: A38792
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPFF-SSGYGRV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE--FLNDFVYK 111
                                                                                                                                                                                                                                                                                                                                                                                                 64
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R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; WUID:95208357; PMID:7900426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 LIYOLPQFKVAAARLINSQNPGMNLTASDVYNLMVMASFEL----NARPFSNWINAFIQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IT-----ARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPF---CDLFTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 FGVADLLP-----FGANQSHQTGTDMYTRYSTLFEGGD-VPFVRAAGDQRV
                                                                                                                                                                                                                                                                                                                       -----TSNWGPYDPFFPVEPYAA-
                                                                                                                                                                                                                                                                                                                                                                157 VDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN-EVDGDESTTWLGVFAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHMTVEKLACSGKEA-----VRVLVNDAVQPLEFCGGVDGV-CELSAF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 GGHLTIERLSCOATALSDEGTYVRLVINEAVLPFNDCTSGPGYSCPLANY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLT-LLNQGPKEA----
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                                                                                                                                                               Length 479;
                                                                                                                                                           15.0%; Score 348; DB 1; L 27.2%; Pred. No. 2.5e-20; iive 70; Mismatches 158;
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A, Gene: SGD: PHO3; MIPS: YBR092c
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         192 -CNINICP
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A,Molecule type: DNA
A,Residues: 1-467 <FB2>
A,Cross-references: EMBL:235962; NID:9536364; PIDN:CAA85046.1; PID:9536365; GSPDB:GN0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: DESCAL
A;Accession: DNA
A;Residues: 1-44 <TAI>
R;Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A;Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A;Reference number: A25367; MUID:87064526; PMID:3023927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-2, YY, 4-43, TY, 45-51 cBER>
R;Silve, S.; Monod, M.; Hinnen, A.; Haguenauer-Teapis, R.
Mol. Cell. Biol. 7, 3306-3314, 1987
A; Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin
A; Reference number: A27774; MUID:88038886; PMID:3313013
                                                                                                                                                                                                                                                                                 AAR
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A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Fesdidues: 1-30 'T',32-51,'S',53-75 <MEX>
A;Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
A;Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
A;Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHOS/PHO3 gene cluster within
A;Reference number: A93074; MUID:87064474; PMID:3537710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a tandem duplicat
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C; Superfamily: yeast acid phosphohistidine; phosphoprotein; phosphoric monoester hydrola
C; Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F;1-17/Domain: signal sequence #status predicted <SIG>
F;1-17/Domain: acid phosphatase, repressible #status experimental <MAT>
F;15-Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval F;337/Active site: His #status predicted
                                                                                                                                                                                                          A;Accession: A00777
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-35, 'Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467
A;Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
A;Accession: A38793
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Nucleic Acida Res. 11, 1657-1672, 1983
A;Title: The nucleotide sequence of the yeast PHOS gene: a putative precursor A;Reference number: A00777; MUID:83168913; PMID:6300772
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                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 18-26, 'X', 28 <ARI2>
R;Mesidues: 18-36, 'X', 28 <ARI2>
R;Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
BENBO J. 1, 675-680, 1982
A;Title: Two yeast acid phosphatase structural genes are the result A;Reference number: $41855; MUID:84236032; PMID:6329697
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A, Molecule type: DNA
A, Residues: 1-51, 'S', 53-60 <SIL>
A, Cross-references: GB:M17306
C, Genetics:
C, Genetics: MIPS:YBR093C
A, Cross-references: SGD:S0000297; MIPS:YBR093C
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27.5%;
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A; Molecule type: DNA
A; Residues: 1-218, 'MXC', 222-467 < BAJI>
A; Cross-references: EMBL:X01080, NID:94148; PIDN:CAA25557.1; PID:9758281
A; Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue;
R; Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
MOI. Cell. Biol. 6, 1855-1865, 1986
A; Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within the A; Reference number: A93074; MUID:87064474; PMID:3537710
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A;Cross-references: UNIPROT:P24031; EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g4760:
A;Cross-references: UNIPROT:P24031; EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g4760:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H:; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
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C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phosphohistidine; phosphoprotein; phosphoric monoester hydrolast
C;Reywords: glycoprotein; phosphohistidine; predicted <SIG>
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphohistidine intermediate) #status predicted
F;53Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,122,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covals
F;337/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.Alternate names: acid phosphatase PHO3, protein YBR0813, protein YBR092c (;Species: Saccharomyces cerevisiae)
N.Alternate names: acid phosphatase PHO3, protein YBR0813, protein YBR092c (;Species: Saccharomyces cerevisiae)
C;Date: 30-Sep-1991 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S48255; S45960; S05794; A25241; S44674 #text_change 09-Jul-2004
R;Mannhaupt, G; Sucka, R: Ehnle, S.; Vetter, I.; Feldmann, H.
A;Act 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1.467 cFE2>
A;Cross-references: EMBL:235961; NID:9536362; PIDN:CAA85045.1; PID:9536363; GSPDB:GN0000.
A;Cross-references: EMBL:235961; NID:9536362; PIDN:CAA85045.1; PID:9536363; GSPDB:GN0000.
A;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast A;Reference number: S05794; MUID:85037940; PMID:6093051
--NEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPF 243
                                                                                                                                                                                                         DTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQ 303
                                                                                                                                                                                                                                                                      304 AVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 WVDSKLVPFSGH-------MTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGV- 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KVWLSFTHDTDILNFLTTAGIID------DKNNL 357
                                                       211 ACNS-CPAMDYDANDDIVNEYDTTYL----DDIAKRLNKENKGLNLTSTDASTLFSWCAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
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C;Accession: $53476; JC1018
R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac)
submitted to the EMBL Data Library, February 1994
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-467 < BUS>
A; Residues: 1-467 < BUS>
A; Cross-references: UNIPROT: P35842; EMBL: L28920; NID: g1616966; PIDN: AAC09508.1; PID: g4561
A; Cross-references: UNIPROT: P35842; EMBL: L28920; NID: g1616966; PIDN: AAC09508.1; PID: g4561
A; Chen, J.X.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A; Title: The primary structure of acid phosphatase gene PHO11 in S. cerevisiae and compan A; Reference number: JC1018
A; Reference number: JC1018
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Cisuperfamily: yeast acid phosphatase
Ciseywords: glycoprotein; phospholistidine; phosphoprotein; phosphoric monoester hydrolast
Fill-17-Domain: signal sequence #status predicted <MAT>
Fil8-467/Product: acid phosphatase #status predicted <MAT>
Fil8-467/Product: Acid phospholistidine intermediate) #status predicted
Fil74/Active site: Acid (phospholistidine intermediate) #status predicted
Fil97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                               TDIINYLTTAGLIDDTRNLTTNHVPFRDHSYHRSW----YIPQGARVYTEKEQCSNDSYV 395
                                                                                                                                                                                                             D------LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVD 158
                                                                                                                                                                                                                                                                  120 DESILEMETTLONSIDVLNPYTGEMNAKRHAREFLAKYGKLMENCTNPPIFTTNSKRIYD 179
                                                                                                                                                                                                                                                                                                                                   SSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN---EVDGDESTTWLGVFAPN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 YGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 NTMVPIFAALGLFN----ATALDPLKPDE-NRLWVDSKLVPFSGHMTVEKLACSGKEAV 389
                                                                                          CTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE----FLNDFVYKFGVA 115
acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein YARO71w
Cispecies: Saccharomyces cerevisiae
Cispecies: Os-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                            180 TAQYFAEALGDGFNIS-LQTLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    I TARLINAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 YQNGPGYKL--IKSIG-----ANLFNATVKLIRQSAH------LDQKVWLSFTHD
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A;Residues: 1-16,'L',18-149,'H',151-353,'Q',355-422,'G',424-467 <CHE>
A;Note: this paper is in Chinese, with an English abstract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 RYVVNDAVVPIESCSSGPGFSCEEGTFYE---YAKDRLRG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG 428
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A,Cross-references: SGD:S000094; MIPS:YAR071w
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Best Local Similarity 24.1*
Matches 115; Conservative
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C;Species: Saccharcmyces cerevisiae
C;Species: Saccharcmyces cerevisiae
C;Accession: S52495; #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52495; Barguence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52495; S67556
R;Andre, B.; Vissers, S.; Urrestarazu, I.
A;Bandre, B.; Vissers, S.; Urrestarazu, I.
A;Bandre, B.; Vissers, S.; Urrestarazu, I.
A;Reference number: S52492
A;Accession: S52495
A;Accession: S52495
A;Accession: S52495
A;Accession: S52495
A;Accession: S52495
A;Cossion: S1488 AND>
A;Cossion: S1488 AND>
A;Cossion: S1488 AND>
A;Cossion: S1488 AND>
A;Cross-references: UNIPROT:P52290; EMBL:Z48432; NID:g683669; PIDN:CAA88335.1; PID:g6836
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                                                                                             19;
                                                                                                                                                                                                                                                                                                           64 CEMKQLQMLARHGERYPTYSKGATIMKTWYKLSNYTRQFNGSLSFLND-DYEFFIRDDDD 122
                                                                                                                                                                                                                                                                                                                                                                                               ------LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCP--NEVDGDE----STTWLGVFAPN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 IAKKLNKENKGLNLTSKDANTLFAMCAYE-LNARGYSDVCDIFTEDELVRYSYGQDLVSF 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 NTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGH-------MTVEKLA 382
                                                                                                                                                                                                                                                                        60 CTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVAD--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 LEMETTPANSDNVLNPYTGEMDAKRHAREFLAQYGYMFENQTSFPIFAASSERVHDTAQY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 ITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKY 275
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                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
                                  Length 467;
                                                                                          Indels
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                                                                                                                                                  21 STOFSFVAAQL----PIP---AQNTSNWGPYDPFFPVEPYAAP-
                               14.4%; Score 335.5; DB 1; 26.3%; Pred. No. 2.5e-19; ive 63; Mismatches 186;
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R; Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67535
A;Accession: S67556
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                        Query Match
Best Local Similarity 26.3
Matches 124; Conservative
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cispecession: A86239
Cispecies: Ascession: A86239
Cispecies: Ascession: A86239
Cispecession: A86239
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A;Cross-references: UNIPROT:004509; GB:AE005172; NID:g2160177; PIDN:AAE60740.1; GSPDB:GNC
C;Genetics:
A;Map position: 1
C;Superfamily: yeast acid phosphatase
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                                                                                                                                                                             174 NRCHDTAQYFIDGLGDKFN----ISLQTISEAESAGANTLSAHHSCPAWDDDVNDDILKK 229
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        : | : | : | : | : | 134
114 BFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD------SKLVPFSGHM 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
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23.2%; Pred. No. 2.7e-05;
tive 58; Mismatches 169;
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Best Local Similarity 23.24
Matches 94; Conservative
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submitted to the EMBL Data Library, February 1994
A; Reference number: 846671
A; Recession: 848996
A; Molecule type: DNA
A; Residues: 1-467 < MAC>
A; Cross-references: UNIPROT: P38693; EMBL: U00029; NID: 9551322; FIDN: AAB69729.1; PID: 94589
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N;Alternate names: protein YHR215w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48996; S59659
                                                                                                                       154 ORVVDSSTNWTAGFGDASGETVLPTLQVVLQEE---GNCTLCNNMCP---NEVDGDESTT
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A;Reference number: S59658
A;Accession: S59659
A;Molecule type: DNA
A;Residues: 1-16,'L',18-81,'AR',84-149,'H',151-467 <XUL>
A;Cross-references: EMBL:U19789; NID:9847755; PIDN:AAA73479.1; PID:9847755
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13.4%; Score 312.5; DB 2;
Best Local Similarity 24.1%; Pred. No. 1.8e-17;
Matches 115; Conservative 66; Mismatches 196;
14 LVNAGTIPLGKLSDIDKIGTQTEIFPFLGGS----
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A;Map position: BR
Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase
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329 YADFSHDNTMVPIFAALGLFNATALD--------PLKPDENRLWVDSKLVPFS 373 | : | : | : | : | : | 320 -LRFAHAETIVPFSCLLGLF----LDGSBFEKIQKEKPLELPPQPPKTRDFRGSTMAPFG 374 8 8

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Search completed: May 27, 2005, 08:34:48 Job time : 43 secs

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Sequence 24, Appl
Sequence 7, Appli
Sequence 11099, A
Sequence 1129, Appl
Sequence 1122, Appl
Sequence 1121, App
Sequence 1118, App
Sequence 137, App
Sequence 26, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 28, Appl
                                                                                                                                                           (without alignments)
1066.499 Million cell updates/sec
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2325
1 MVSSAFAPSILLSIMSSLAL.....TYARENGQGDFAKCGFVPSE 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US11NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US11NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US11NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US11NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                                                                                                                                     May 27, 2005, 08:33:17; Search time 142 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-083-452-7
US-10-034-510-7
US-10-732-923-11099
US-10-358-960-2
US-10-442-538-122
US-10-442-538-145
US-10-732-923-11118
US-10-732-923-11118
US-10-732-923-11100
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US-10-999-214-28
US-10-083-452-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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10-734-61	8-10-134-310-4 6-10-732-633-11	S-10-442-538-119	-10-442-538-14	-10 - 442 - 538 - 11	-442-538-14	-09-999-214-3	-10-083-452-	10-734-510-	-10-732-923-1	-10-442-538-12	-09-999-214-2	-10-083-452-	10-734-510-6	-10-732-923-11	-10-442-538-14	-10-442-538-12	-10-442-538-14	-10-442-538-12	-10-442-538-16	-10-442-538	-10-442-538-16	-10-492-782-4	-10-492-782-	-10-492-782-	-10-492-782-2	2-782-2	-10-492-782-	-10-492-782-3	-10-442-538-11	-538-1	-10-442-538-15	
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ALIGNMENTS

CORRECTOR APPLICATION US/0999214
Publication No. US20030064497A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Bostergaard, Peter R.
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: 09/482,558
PRIOR FILING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-03-18
PRIOR PELING DATE: 1997-05-07

LENGTH: 439 TYPE: PRT ORGANISM: Peniophora lycii FEATURE:

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GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
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                                                                                                             1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC
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     Query Match 100.0%; Score 2325; DB 13; Length 439; Best Local Similarity 100.0%; Pred. No. 1.8e-216; Matches 439; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 2325; DB 16; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.8e-216;
Matches 439; Conservative 0; Mismatches 0; Indels 0;
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TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618-560-018
FURENT PELICATION NUMBER: US/10/734,510
CURRENT PELICATION NUMBER: US/09/273,811A
PRIOR APPLICATION NUMBER: US/09/273,811A
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-31
PRIOR PELING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
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; ORGANISM: Peniophora ycii
US-10-734-510-7
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                                                                                                                                                                Gaps
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0
                                                                                                        ; Score 2325; DB 10; Length 439;
; Pred. No. 1.8e-216;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
ADPLICANT: Svendeen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REPERENCE: $618.500-03
CURRENT APPLICATION NUMBER: US/09/273,871
PRIOR PILING DATE: 1999-03-22
PRIOR PLING DATE: 1998-03-22
PRIOR PLING DATE: 1998-03-22
PRIOR PLING DATE: 1998-03-23
PRIOR PLING DATE: 1998-03-23
PRIOR PLING DATE: 1998-03-23
PRIOR PLING DATE: 1998-03-23
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR PLING DATE: 1998-09-18
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PRAESEQ FOR WINGOME VERSION 4.0
SEC ID NOS: 15
LENGTH: 439
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                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 439; Conservative 0
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-09-999-214-24
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361 NRLWYDSKLYPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TSGARSRQVAAVAKIQMARPFTDPRYZEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY
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                                                                               301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDE
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                                                                                                                                                                                                                                                                                                                                        Squence 2, Application US/10358960
Publication No. US20030208788A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mateni, Tomoko
APPLICANT: Fuglsang, Claus
APPLICANT: Fuglsang, Claus
APPLICANT: Fukuyama, Alian
APPLICANT: Fukuyama, Shiro
ITILE OF INVENTION: Phytase Variants
FILE REFERENCE: 10261.200-US
CURRENT APPLICATION NUMBER: US/10/358,960
CURRENT FILING DATE: 2003-02-05
NUMBER OF SECIL DOS: 14
                                                                                                                                                                                                                                      421 YARENGQGDFAKCGFVPSE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
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CRGANISM: Peniophora lycii
US-10-358-960-2
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   1 MVSSAFAPSILLISLMSSIALSTQFSFVAAQLBIPAQNTSNWGPYDPFFPVEPYAAPPEGC
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; Publication No. US20050108791A1
; Fublication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICATT Edgerton, Michael D
; TITLE OF INVENTION: TRANSCHIC PLANTS WITH IMPROVED PHENOTYPES
; CURRENT PELLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11099
; LENGTH: 439
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US-10-732-923-11099
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PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 145
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                                                                                                                                                                          Best Local Similarity 100.
Matches 409; Conservative
                                                                                                                                                                        Similarity
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US-10-442-538-145
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96.3%; Score 2238; DB 15; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.5e-208;
Matches 419; Conservative 0; Mismatches 0; Indels 0
                                              Sequence 122, Application US/10442538
Publication No. US20030224491A1
GENERAL INFORMATION:
APPLICANT F. Hoffmann-La Roche AG
ITTLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
FILE REFERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/10/442,538
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: EP 00121663.9
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PERENTIN Ver: 2.0
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Publication No. US20030224491A1
GERREAL INFORMATION:
I APPLICANT: F. Hoffmann-La Roche AG
TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
FILE REFERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/10/442,538
CURRENT PLING DATE: 2003-05-20
FRIOR APPLICATION NUMBER: US/09/684,855
FRIOR APPLICATION NUMBER: EP 90121663.9
FRIOR APPLICATION NUMBER: EP 90120289.6
FRIOR APPLICATION NUMBER: EP 99120289.6
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; ORGANISM: P. lycii
US-10-442-538-122
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                                    US-10-442-538-122
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                                                                                                                                          1 LPIPAQNTSNWGPYDPFFPVEPYBAAPBGGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK
                                                                                                                                                                                                                                                                                                                        151 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG
                                                                                                                                                                                                                                                                                                                                                    211 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA
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                                                                                                           31 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK
                                                                                                                                                                                                                  91 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA
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                                                          Gapa
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Publication No. US20050108791A1

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: EGGETCON, Michael D

ITILE OF INVENTION:

FILE REFERENCE: 38-15(52796)C

CURRENT APPLICATION UNMERR: US/10/732,923

CURRENT APPLICATION NUMBER: US/310,154

PRIOR APPLICATION NUMBER: 10/310,154

PRIOR APPLICATION NUMBER: 10/310,154

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 11118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 94.2%; Score 2189; DB 17; Length 409; Best Local Similarity 99.8%; Pred. No. 2.5e-203; Matches 408; Conservative 1; Mismatches 0; Indels 0.
     Length 409;
                                                          Indels
94.2%; Score 2191; DB 15;
100.0%; Pred. No. 1.6e-203;
tive 0; Mismatches 0;
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                                                                                                                                                                                                              384 -----SGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFVESQTYAREN 425
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                                                                                                                                    309 NRTFYADFSHDNOMVAIFSAMGLFNOSAPLDPSXPDPNRTWVTSKLVPFSARMVVERLXC
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APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Gostergaard, Peter R.
APPLICANT: Ostergaard, Peter R.
TILLE OSTERVENTON: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT FILING DATE: 2000-01.13
PRIOR FILING DATE: 2000-01.13
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 08/993,359
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-05-07
PRIOR FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09999214 Publication No. US20030064497A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Paxillus involtus
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Best Local Similarity 55.34
Matches 242; Conservative
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                                                                                                                                                                                                                                                                                                                  426 GQGDFAKCGFVP 437
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-999-214-26
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                        181 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEVVSYEYYY 240
                                                                                                                                                                                                            DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 330
                                                                                                                                                                                                                                       241 DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 300
                                                                                                                                                                                                                                                                                                                  DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHMTVEKLACSGKEAVR 390
                                                                                                                                                                                                                                                                                                                                           301 DFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 XWLAVFAPPITARLNAAAPGANLTDXDAXNLXXLCPFETVSXEXXSXFCDLFEXXPEEFX 248
                                                                                                      211 VFAPNITARLMAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYY 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 TWLGVFAPNITARLINAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLF--TAEEYV 264
AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AAQLPIPXQXQXXWSPYSPYFPVAXYXAPPAGCQIXQVNIIQRHGARFPTSGAATRIQAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAA
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.9%; Score 1347; DB 15; Length Best Local Similarity 61.8%; Pred. No. 1.4e-121; Matches 267; Conservative 32; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: P. HOFFmann-La Roche AG
TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS;
FILE REFERENCE: C38435/11652
CURRENT APPLICATION NUMBER: US/10/442,538
CURRENT PILING DATE: 2003-05-20
PRIOR PELING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 1200-10-10
PRIOR PILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PRECEIN OFFER PRIOR PILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SEQ ID NOS: 169
SEQ ID NOS: 169
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NAME/KEX: UNSURE
LOCATION: (1)..(442)
OTHER INFORMATION: n is unknown
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OTHER INFORMATION: x is unknown
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ORGANISM: Basidio
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420 VESQTFARSDGAGDFEKC 437

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181 VVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMD 239

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358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV 416
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52.6%; Pred. No. 1.7e-107;
ative 61; Mismatches 128;
                                                                                                                                                                     APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Breinholt, Jens
CURRENT APPLICATION WUMBER: US/09/999, 214
CURRENT FILING DATE: 2000-01-13
FRIOR APPLICATION WUMBER: 09/482,558
FRIOR APPLICATION WUMBER: 08/993,359
FRIOR FILING DATE: 1997-12-19
FRIOR APPLICATION WUMBER: 0301/97
FRIOR APPLICATION WUMBER: 0529/97
FRIOR APPLICATION WUMBER: 0529/97
FRIOR APPLICATION WUMBER: 1388/97
FRIOR FILING DATE: 1997-02-07
FRIOR APPLICATION WUMBER: 1388/97
FRIOR FILING DATE: 1997-12-01
FRIOR APPLICATION WUMBER: 60/046,082
FRIOR FILING DATE: 1997-05-07
FRIOR APPLICATION WUMBER: 60/046,082
FRIOR FILING DATE: 1997-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                          US-09-999-214-28
. Sequence 28, Application US/09999214
. Publication No. US20030064497A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Paxillus involtus
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; LOCATION: (1)...(19)
US-09-999-214-28
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Matches 230;
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Best Local
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298 ARLIGGAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL 356
                                                                                                                                                                                                                                                415
                                                                                                                                                                                                                                                                      360 VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCGGDRNGLCTLAKF 419
                                                               240 MCPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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Sequence 11101.
Publication No. US20050108791A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
FILE REFERENCE: 38-15(52796)C
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 11100
LENGTH: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.8%; Score 1204; DB 17; Length 442; Best Local Similarity 55.3%; Pred. No. 1.1e-107; Matches 242; Conservative 51; Mismatches 139; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: cf. Ceriporia sp. CBS 100231
US-10-732-923-11100
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                       62 VTQVNLIQRHGARWPISGARSRQVAAVAKIQMARPFIDPKYEFLNDFVYKFGVADLLPFG
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                                                                                                                                                         SQUENCE 4. Application US/10083452
Publication No. US20020127218A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Phyrase Variants
FILE REFERENCE: 5618 500-03
CURRENT APPLICATION NUMBER: US/10/083,452
CURRENT FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-01-22
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR PILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SEOFURARE: FASESEQ FOR WINGOWS VETSION 4.0
SEQ ID NO 4
LENGTH: 442
                                                     417 ESQTYARENGOGDFAKC 433
                                                                                  421 ESQAYARSGGAGDFEKC 437
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Matches 230; Conserve
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US-10-083-452-4
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                                                                        TITLE OF INVENTION: Phytase Variants
FILE REPERENCE: 5618-500-02
FILE REPERENCE: 5618-500-03
CURRENT APPLICATION NUMBER: US/10/734,510
CURRENT FILING DATE: 2003-12-12
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-31
PRIOR FILING DATE: 1998-06-31
PRIOR FILING DATE: 1998-06-35
NUMBER OF SEQ ID NOS: 15
SEQ ID NOS: 15
Sequence 4, Application US/10734510 Publication No. US20040175376A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         18; Gaps
                         Sequence 11101, Application US/10732923

Publication No. US20550108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52795)

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT PILING DATE: 2003-12-10

PRIOR PILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 11101

LENGTH: 442

TYPE: PRI
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US-10-732-923-11101
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ESQAYARSGGAGDFEKC 437
RESULT 15
US-10-732-923-11101
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Search completed: May 27, 2005, 08:46:20 Job time : 144 secs

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Sequence 2, Appli
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762.115 Million cell updates/sec
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Sequence 18, A
Sequence 118, A
Sequence 17, A
Sequence 11, A
Sequence 30, Ap
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUG_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUG_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-083-482-558A-24
US-10-083-452-7
US-09-684-855-145
US-09-684-855-145
US-09-684-855-145
US-09-684-855-137
US-09-993-359-26
US-09-482-558A-26
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S-09-482-558A-30
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Maximum Match 100%
Listing first 45 summaries
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28 1155.5 49.7 420 4 US-09-488-265B-19 Sequence 19, Appl 29 1153 49.6 453 3 US-08-993-359-22 Sequence 22, Appl 30 1153 49.6 453 4 US-09-273-871A-6 Sequence 22, Appl 31 1153 49.6 453 4 US-09-481-258A-22 Sequence 22, Appl 33 1150 49.5 453 4 US-09-684-855-143 Sequence 6, Appli 34 1149 49.4 435 4 US-09-684-855-143 Sequence 121, Appl 36 1148 49.4 435 4 US-09-684-855-121 Sequence 121, Appl 37 1144.5 49.2 369 4 US-09-684-855-123 Sequence 121, Appl 38 1144.5 49.2 369 4 US-09-684-855-123 Sequence 123, Appl 39 941.5 40.5 467 4 US-09-684-855-123 Sequence 123, Appl 40 13.5 35.8 467 4 US-09-684-855-169 Sequence 24, Appl 40 13.5 35.8 467 4 US-09-684-855-139 Sequence 139, Appl 42 831.5 35.8 467 4 US-09-684-855-139 Sequence 139, Appl 42 831.5 35.8 467 4 US-09-684-855-139 Sequence 139, Appl 42 831.5 35.8 467 4 US-09-684-855-139 Sequence 139, Appl 43 831.5 35.8 467 4 US-09-684-855-139 Sequence 139, Appl 43 830.5 35.7 467 4 US-09-684-855-163 Sequence 163, Appl 44 830.5 35.7 467 4 US-09-684-855-163 Sequence 163, Appl 45 Handward 163, Appl 45 Handward 163, Appl 46 Handward 163, Appl 47 Handward 163, Appl 47 Handward 163, Appl 48 Handward 163, Appl 48 Handward 163, Appl 47 Handward 163, Appl 48 Handward 163, Appl
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100.0%; Pred. No. 2.7e-250;
tive 0; Mismatches 0;
                                                                                 GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Bechnol, Anders
APPLICANT: Breinhol, Loss
APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT PAPLICATION NUMBER: US/08/993,359A
CURRENT PLING DATE: 1997-12-18
EARLIER PILING DATE: 1996-12-20
EARLIER PILING DATE: 1996-12-20
EARLIER PILING DATE: 1996-12-20
EARLIER FILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-05-07
EARLIER PILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
RESULT 1
18-08-393-359-24
Sequence 24, Application US/08993359A
Patent No. 6039942
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Best Local Similarity 100.
Matches 439; Conservative
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LENGTH: 439
TYPE: PRT
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                                                            VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
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CITY: New York
STATE: NY
                                                                               361 NRLWYDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Ohmann, Anders
APPLICANT: Ohmann, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5101.200-US
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CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
RILING DATE: 12-DEC-1997
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTONEY/AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                           421 YARENGQGDFAKCGFVPSE 439
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09221654
Patent No. 6054306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gregg, Valeta A
REGIESTRATION UNUBER: 35,127
REFERENCE/DOCKET NUMBER: 5101
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX.
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LENGTH: 439 amino acids
TYPE: amino acid
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                                                                                                                                          Length 439;
                                                                                                                                                                                           Indels
                                                                                                                                    Query Match 100.0%; Score 2325; DB 3; Best Local Similarity 100.0%; Pred. No. 2.7e-250; Matches 439; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Diskette
COMPUTER: IEM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTWARE: FRASTSQ for Windows Version 2.0
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APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Puglsang, Claus
APPLICANT: Onmann, Anders
APPLICANT: Ostergaard, Peter
ITILE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/989,358A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1481/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08989358A Patent No. 6060298
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STRANDEDNESS: single
                                                   ; MOLECULE TYPE: protein US-09-221-654-2
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PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR PELICATION NUMBER: PA 1999 00091
PRIOR PELING DATE: 1999-01-22
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-06-25
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US-09-273-871A-7
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Patent No. 6514495
GENERAL INPORMATION:
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618-500-0S
CURRENT APPLICATION NUMBER: US/09/273,871A
CURRENT FILING DATE: 1998-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR PILING DATE: 1998-03-23
PRIOR PLING DATE: 1998-06-19
                                                                                                                  REFERENCE/DOCKET NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATYONEY/ABENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
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181 VVLQEEGNCTI.CNNMCPNEVDGDESTT#LGVFAPNI.TARLNAAAPSANLSDSDALTLAMM 240
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Patent No. 6569659

GENERAL INPORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Offinann, Anders
APPLICANT: Puglsang, Claus C.
APPLICANT: Predisang, Claus C.
APPLICANT: APPLICANTON NUMBER: US/09/993,359
PRIOR APPLICATION NUMBER: 1480/96
PRIOR APPLICATION NUMBER: 1480/96
PRIOR APPLICATION NUMBER: 1481/96
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ
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100.0%; Pred. No. 2.7e-250;
ative 0; Mismatches 0;
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Sequence 122. Application US/09684855

Patent No. 6599735

GENERAL INFORMATION:

TITLE OF INVENTION: CONTINUOUS FERMENTATION PROFICE TITLE OF INVENTION: CONTINUOUS FERMENTATION PROFICE TO FILE REFERENCE: C38435/111692

CURRENT APPLICATION NUMBER: US/09/684,855

CURRENT FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: EP 99120289.6

PRIOR PILING DATE: 1999-10-11

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 122

LENGTH: 419
    PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR PELING DATE: 1998-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR PILING DATE: 1999-01-23
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR APPLICATION NUMBER: 60/080,675
PRIOR APPLICATION NUMBER: 60/090,675
PRIOR PILING DATE: 1998-06-25
NUMBER: OF SEQ ID NOS: 15
SEQ ID NO 7
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Best Local Similarity 100.
Matches 439; Conservative
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US-10-083-452-7
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ORGANISM: P. lycii
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PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 0301/97
PRIOR PILIG DATE: 1997-03-18
PRIOR PILIG DATE: 1997-03-18
PRIOR FILING DATE: 1997-05-07
PRIOR FILING DATE: 1997-05-07
PRIOR FILING DATE: 1997-05-07
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-05-09
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 439
TYPE: PRT
ORGANISM: Peniophora lycii
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GENERAL INFORMATION:
GENERAL INFORMATION:
FILE OF INVENTION: Phytase Variants
FILE OF INVENTION: Phytase Variants
FILE OF INVENTION: Phytase Variants
FILE OF INVENTION NUMBER: US/10/083,452
CURRENT APPLICATION NUMBER: US/09/273,871
FRIOR PRILING DATE: 1999-03-22
PRIOR FILING DATE: 1998-03-23
FRIOR FILING DATE: 1998-03-33
FRIOR FILING DATE: 1998-06-19
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; LOCATION: (1)...
US-09-482-558A-24
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US-10-083-452-7
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91 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 150
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                                              241 EEYVSYEYYYDLDKYYGTGPGNALGPVGGVGYVNELLARLTGGAVRDETQTNRTLDSDPA 300
                                                                                                                                                   TFPLMRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 360
                                                                                                                         TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LPIPAQNTSNWGPYDPFFPVBPXAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 LPIPAQNTSNWGPYDPFPPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK
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TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
FILE REPERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/09/684,855
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: EP 00121663.9
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: EP 99120289.6
PRIOR APPLICATION NUMBER: EP 99120289.6
PRIOR APPLICATION NUMBER: 199-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTING DATE: 199-10-11
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94.2%; Score 2191; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 2.2e-235;
Matches 409; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145, Application US/09684855; Patent No. 6599735; GENERAL INFORMATION:
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Patent No. 6599735
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ORGANISM: P. lycii
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US-09-684-855-145
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                                                                                                                                                                                                                                                                             61 RSRQVAAVAKIQMARPFIDPKYEFINDFVYKRGVADLLPFGANQSHQTGTDMYTRYSTIF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
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                                                                                                                                                                          1 STQFSFVAAQLFIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA
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                                                                                                                                                 21 STOPSFVAAQLPIPAQNTSNWGPYDPFPPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA
                                                                                                                                                                                                                                                                                                                                              141 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV
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                                              96.3%; Score 2238; DB 4; Length 419; 100.0%; Pred. No. 1.3e-240; ive 0; Mismatches 0; Indels
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Patent No. 6720174
GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Improved Phytases
FILE REFERENCE: 5808.200-03
FULE REFERENCE: 2000-01-20
NUMBER OF SEQ ID NOS: 98
SOFTMARE: PatentIn version 3.2
SEQ ID NO 2.1
LENGTH: 419
                                         Query Match 96.3%
Best Local Similarity 100.0
Matches 419, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Peniophora lycii
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US-09-488-265B-21
US-09-684-855-122
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US-08-993-359-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VAKLQSAXXXTDPKLDFLXNXTYXLGXDDLVPFGAXQSSQAGQBAFTRYSXLVSXDNLPF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 NRTFYADFSHDNTWVPIFAALGLFNATA-LDPLKPDENRLWVDSKLVPFSGHMTVEKLAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 ------SGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFVESQTYAREN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 VRAAGDORVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGD-EST 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 TWLGVFAPNITARINAAAPSANLSDSDALTIMDMCPFDTLSSGNASPFCDLF--TAEEYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AAQLPIPXQXQXXWSPYSPYFPVAXYXAPPAGCQIXQVNIIQRHGARFPTSGAATRIQAA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.9%; Score 1347; DB 4; Length 442; Best Local Similarity 61.8%; Pred. No. 4e-141; Matches 267; Conservative 32; Mismatches 111; Indels 2
              APPLICANT: F. HOFFmann-La Roche AG
TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS;
FILE REFERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/09/684,855
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: EP 90121663.9
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08993359A
Patent No. 6039942
GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Dech, Lisbeth
APPLICANT: Ohmann, Anders
APPLICANT: Perinholt, Jens
APPLICANT: Fuglsang, Claus C.
APPLICANT: Ostergaard, Peter R.
                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Basidio
FEATURE:
NAMM-KRE: UNSURE
COCATION: (1)...(442)
OTHER INFORMATION: n is unknown
LOCATION: (1)...(442)
COTHER INFORMATION: x is unknown
US-09-684-855-137
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GENERAL INFORMATION:
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                                                                                                                                                                                                                    LENGTH: 442
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61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYBFLNDFVYKFGVADLLPF 120
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TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/08/993,359A
CURRENT FILING DATE: 1997-12-18
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
EARLIER PELLING DATE: 1996-12-20
EARLIER PELLING DATE: 1996-12-20
EARLIER PELLING DATE: 1997-03-18
EARLIER PILLING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-02-01
EARLIER FILING DATE: 1997-02-01
EARLIER FILING DATE: 1997-02-01
EARLIER PILLING DATE: 1997-02-01
EARLIER PILLING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FABSEE FABSEQ for Windows Version 3.0
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WS-09-482-558A-26
Sequence 26, Application US/09482558A
Patent No. 6569659
GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
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US-08-993-359-28
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APPLICANT: Fuglsang, Claus C.
APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/09/482,558A
CURRENT FILING DATE: 100-01-13
PRIOR FILING DATE: 1997-12-18
PRIOR FLING DATE: 1996-12-20
PRIOR PLING DATE: 1997-03-18
PRIOR PLING DATE: 1997-03-18
PRIOR PLING DATE: 1997-03-18
PRIOR PILING DATE: 1997-03-18
PRIOR PILING DATE: 1997-03-18
PRIOR PILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-05-07
PRIOR PILING DATE: 1997-05-07
PRIOR PILING DATE: 1997-05-09
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ORGANISM: Paxillus involtus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-482-558A-26
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Sequence 28, Application US/08993359A Patent No. 6039942 GENERAL INFORMATION:

US-08-993-359-28

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; Mismatches 128;
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
APPLICANT: Puglaand, Claus C.
APPLICANT: Puglaand, Claus C.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/08/993,359A
CURRENT APPLICATION NUMBER: 1480/96
EARLIER APPLICATION NUMBER: 1480/96
EARLIER PILING DATE: 1996-12-20
EARLIER PELING DATE: 1996-12-20
EARLIER PELING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-03
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US-09-273-871A-4
; Sequence 4, Application US/09273871A
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Matches 230; Conservative
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LOCATION: (1)...(19)
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APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
CURRENT APPLICATION NUMBER: US/09/273,871A
CURRENT FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-25
PRIOR FILING DATE: 1998-01-25
PRIOR FILING DATE: 1998-06-55
PRIOR FILING DATE: 1998-06-55
PRIOR FILING DATE: 1998-06-55
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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Sequence 28, Application US/09482558A
Sequence 28, Application US/09482558A
GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Libbeth
APPLICANT: Breinholt, Jens
APPLICANT: Breinholt, Jens
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Paxillus involtus
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122 ANOSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
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                                                                     CURRENT PELICATION NUMBER: US/09/482,558A
CURRENT FILING DATE: 2000-01-13
PRIOR PLING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR PILING DATE: 1997-12-20
PRIOR PILING DATE: 1996-12-20
PRIOR PILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 1481/96
PRIOR PILING DATE: 1996-12-20
PRIOR PELING DATE: 1997-12-00
PRIOR PILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-05-07
PRIOR PILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PASKEEQ fOR WINDOWS VETRION 3.0
APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 27, 2005, 08:34:00 Job time : 45 secs
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Best Local Similarity 52.64
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-482-558A-28
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